In the Specification;

Please amend the Cross-Reference to Related Applications paragraph beginning on line 5 of page 1 as follows:

This application is a continuation-in-part of U.S. Patent Application serial number 09/578,063, filed on May 24, 2000, now U.S. Patent 6,764,677, which is a continuation-in-part of U.S. Patent Application serial number 09/333,159, filed on June 14, 1999, now U.S. Patent 7,033,780.

This application is also a continuation-in-part of U.S. Patent Application serial number 09/596,194, filed on June 16, 2000, now abandoned, which is a continuation-in-part of U.S. Patent Application serial number 09/342,364, filed on June 29, 1999, now abandoned.

This application is also a continuation-in-part of U.S. Patent Application serial number 09/608,452, filed on June 30, 2000, now abandoned, which is a continuation-in-part of U.S. Patent Application serial number 09/393,996, filed on September 10, 1999, now abandoned.

This application is also a continuation-in-part of U.S. Patent Application serial number 09/345,680, filed on June 30, 1999, now abandoned.

The contents of each of the applications cross-referenced in this section are incorporated into this disclosure by reference.

Please amend the paragraphs beginning on line 10 of page 4 to line 17 of page 7 as follows:

The invention also features nucleic acid molecules which are at least 40% (or 50%, 60%, 70%, 80%, 90%, 95%, or 98%) identical to the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, and 82, the human TANGO 273 nucleotide sequence of the cDNA insert of a clone deposited on April 2, 1999 with the American Type Culture Collection® (ATCC®) as accession no. 207185, the murine TANGO 273 nucleotide sequence of the cDNA insert of a clone deposited on April 2, 1999 with ATCC® as accession no. 207221, the human TANGO 325 nucleotide sequence of the cDNA insert of a clone deposited on May 28, 1999 with ATCC® as

accession no. PTA-147, the human TANGO 364 nucleotide sequence of the cDNA insert of a clone deposited on July 23, 1999 with ATCC® as accession no. PTA-425, the human TANGO 405 nucleotide sequence of the cDNA insert of a clone deposited on July 23, 1999 with ATCC® as accession no. PTA-424, ~~the murine TANGO 405 nucleotide sequence of the cDNA insert of a clone deposited on ____ with ATCC® as accession no. ___, the human M019 nucleotide sequence of the cDNA insert of a clone deposited on ____ with ATCC® as accession no. ___~~, or a complement thereof. These deposited nucleotide sequences are hereafter individually and collectively referred to as "the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~."

The invention features nucleic acid molecules which include a fragment of at least 15 (25, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, or 3500 or more) consecutive nucleotide residues of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, or a complement thereof.

The invention also features nucleic acid molecules which include a nucleotide sequence encoding a protein having an amino acid sequence that is at least 50% (or 60%, 70%, 80%, 90%, 95%, or 98%) identical to the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424, ~~___, and ___~~, or a complement thereof.

In certain embodiments, the nucleic acid molecules have the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~.

Also within the invention are nucleic acid molecules which encode a fragment of a polypeptide having the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, the fragment including at least 10 (12, 15, 20, 25, 30, 40, 50, 75, 100, 125, 150, 200, 250, 300, 400, 500, 750, 1000 or more) consecutive amino acid residues of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85.

The invention includes nucleic acid molecules which encode a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-

28, 33-38, 43, 53-55, 63-65, 73, and 83-85, wherein the nucleic acid molecule hybridizes under stringent conditions to a nucleic acid molecule having a nucleic acid sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424, ~~___, and ___~~, or a complement thereof.

Also within the invention are isolated polypeptides or proteins having an amino acid sequence that is at least about 50%, preferably 60%, 75%, 90%, 95%, or 98% identical to the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85.

Also within the invention are isolated polypeptides or proteins which are encoded by a nucleic acid molecule having a nucleotide sequence that is at least about 40%, preferably 50%, 60%, 75%, 85%, or 95% identical to the nucleic acid sequence encoding any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, and isolated polypeptides or proteins which are encoded by a nucleic acid molecule consisting of the nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~.

Also within the invention are polypeptides which are naturally occurring allelic variants of a polypeptide that includes the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes under stringent conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424, ~~___, and ___~~, or a complement thereof.

The invention also features nucleic acid molecules that hybridize under stringent conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424, ~~___, and ___~~, or a complement thereof. In other embodiments, the nucleic acid molecules are at least 15 (25, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, or 3500 or more) nucleotides in length and hybridize under stringent conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12,

21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424, ~~___, and ___,~~ or a complement thereof. In some embodiments, the isolated nucleic acid molecules encode a cytoplasmic, transmembrane, extracellular, or other domain of a polypeptide of the invention. In other embodiments, the invention provides an isolated nucleic acid molecule which is antisense to the coding strand of a nucleic acid of the invention.

Please amend the paragraphs beginning on line 16 of page 12 to line 28 of page 14 as follows:

Figure 1 comprises Figures 1A through [[1J]]1C. ~~The nucleotide sequence (SEQ ID NO: 1) of a cDNA encoding the human TANGO 273 protein described herein is listed in Figures 1A-1C. The ORF (residues 135 to 650; SEQ ID NO: 2) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 3) of human TANGO 273 is listed. The nucleotide sequence (SEQ ID NO: 11) of a cDNA encoding the murine TANGO 273 protein described herein is listed in Figures 1D-1G. The ORF (residues 137 to 652; SEQ ID NO: 12) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 13) of murine TANGO 273 is listed.~~ An alignment of the amino acid sequences of human ("Hum."; SEQ ID NO: 3) and murine ("Mur."; SEQ ID NO: 13) TANGO 273 protein is shown in Figure [[1H]]1A, wherein identical amino acid residues are indicated by ":" and similar amino acid residues are indicated by ".". Figure [[1I]]1B is a hydrophobicity plot of human TANGO 273 protein, and Figure [[1J]]1C is a hydrophobicity plot of murine TANGO 273 protein.

Figure 2 comprises Figures 2A through ~~2M-18~~2H-18. ~~The nucleotide sequence (SEQ ID NO: 21) of a cDNA encoding the human TANGO 325 protein described herein is listed in Figures 2A through 2E. The ORF (residues 135 to 2000; SEQ ID NO: 22) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 23) of human TANGO 325 is listed.~~ Figure [[2F]]2A is a hydrophobicity plot of TANGO 325 protein. An alignment of the amino acid sequences of TANGO 325 ("325"; SEQ ID NO: 23) and Slit-1 protein ("Slit"; SEQ ID NO: 29) protein is shown in Figures ~~2G to 2L~~2B-2G. In Figures 2H-1 to 2H-18~~2M-1 to 2M-18~~, an alignment of the nucleotide sequences of the cDNA encoding human TANGO 325 protein ("325"; SEQ ID NO: 23) and the nucleotide sequence of the cDNA encoding Slit-1 protein ("Slit"; SEQ ID NO: 30) is shown. This

alignment was made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4).

Figure 3 comprises Figures 3A through [[3K]]3C. ~~The nucleotide sequence (SEQ ID NO: 31) of a cDNA encoding the human TANGO 364 protein described herein is listed in Figures 3A through 3E. The ORF (residues 235 to 1764; SEQ ID NO: 32) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 33) of human TANGO 364 is listed.~~ Figure [[3F]]3A is a hydrophobicity plot of human TANGO 364 protein. ~~The nucleotide sequence (SEQ ID NO: 41) of an alternatively-spliced form of the cDNA encoding the human TANGO 364 protein described herein is listed in Figures 3G through 3I. The ORF (residues 2 to 898; SEQ ID NO: 42) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 43) of the protein encoded by the splice variant is listed.~~ Figures 3B and 3C~~3J and 3K~~ are an alignment of the amino acid sequence of SEQ ID NOs: 33 and 43.

Figure 4 comprises Figures 4A through 4H[[4P]]. ~~The nucleotide sequence (SEQ ID NO: 51) of a cDNA encoding the human TANGO 405 protein described herein is listed in Figures 4A through 4C. The ORF (residues 154 to 780; SEQ ID NO: 52) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 53) of human TANGO 405 is listed.~~ Figure 4A[[4D]] is a hydrophobicity plot of human TANGO 405 protein. ~~The nucleotide sequence (SEQ ID NO: 61) of a cDNA encoding the murine TANGO 405 protein described herein is listed in Figures 4E and 4F. The ORF (residues 174 to 707; SEQ ID NO: 62) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 63) of murine TANGO 405 is listed.~~ Figure 4B[[4G]] is a hydrophobicity plot of murine TANGO 405 protein. An alignment of the amino acid sequences of human TANGO 405 protein (SEQ ID NO: 53) and murine TANGO 405 protein (SEQ ID NO: 63) amino acid sequences is shown in Figure 4C[[4H]]. An alignment of the nucleotide sequences of the human (SEQ ID NO: 52) and murine (SEQ ID NO: 62) ORFs encoding TANGO 405 protein is shown in Figures 4D through 4F~~4I through 4K~~. Figure 4G[[4L]] is an alignment of the amino acid sequences of murine TANGO 405 protein ("mT405"; SEQ ID NO: 63) and murine dectin-2 ("Dectin"; SEQ ID NO: 60). Figure 4H[[4M]] is an alignment of the amino acid sequences of human TANGO 405 protein ("hT405"; SEQ ID NO: 53) and murine dectin-2 ("Dectin"; SEQ ID NO: 60). ~~The nucleotide sequence (SEQ ID NO: 71) of an alternative embodiment of a cDNA encoding the murine TANGO 405 protein described herein is listed in Figures 4N, 4O and 4P. The ORF (residues 179 to 805; SEQ ID NO: 72) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 73) of the alternative embodiment of murine TANGO 405 is listed.~~

~~Figure 5 comprises Figures 5A through 5C. The nucleotide sequence (SEQ ID NO: 81) of a cDNA encoding the human M019 (i.e., TANGO 533) protein described herein is listed in Figures 5A and 5B. The ORF (residues 331 to 585; SEQ ID NO: 82) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 83) of human M019 protein is listed.~~ Figure 5A[[5C]] is a hydrophobicity plot of human M019 protein, in which the locations of cysteine residues ("Cys"), and the predicted extracellular ("out"), intracellular ("ins"), or transmembrane ("TM") locations of the protein backbone is indicated by a horizontal bar.

Please amend the paragraph beginning on line 22 of page 15 as follows:

The full length of the cDNA encoding human TANGO 273 protein (~~Figure 1;~~ SEQ ID NO: 1) is 2964 nucleotide residues. The ORF of this cDNA, nucleotide residues 135 to 650 of SEQ ID NO: 1 (i.e., SEQ ID NO: 2), encodes a 172-amino acid transmembrane protein (~~Figure 1;~~ SEQ ID NO: 3).

Please amend the paragraph beginning on line 23 of page 21 as follows:

Figure 1B[[1I]] depicts a hydrophobicity plot of human TANGO 273 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 22 of SEQ ID NO: 3 is the signal sequence of human TANGO 273 (SEQ ID NO: 4). The hydrophobic region which corresponds to amino acid residues 61 to 81 of SEQ ID NO: 3 is the transmembrane domain of human TANGO 273 (SEQ ID NO: 7). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 273 protein from about amino acid residue 100 to about amino acid residue 120 appears to be located at or near the surface of the protein, while the region from about amino acid residue 130 to about amino acid residue 140 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 1 of page 23 as follows:

The full length of the cDNA encoding murine TANGO 273 protein (~~Figure 1;~~ SEQ ID NO: 11) is 2915 nucleotide residues. The ORF of this cDNA, nucleotide residues 137 to 650 of SEQ ID NO: 11 (i.e., SEQ ID NO: 12), encodes a 172-amino acid transmembrane protein (~~Figure 1;~~ SEQ ID NO: 13).

Please amend the paragraph beginning on line 13 of page 23 as follows:

Figure 1C[[1J]] depicts a hydrophobicity plot of murine TANGO 273 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 22 of SEQ ID NO: 13 is the signal sequence of murine TANGO 273. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of murine TANGO 273 protein from about amino acid residue 100 to about amino acid residue 120 appears to be located at or near the surface of the protein, while the region from about amino acid residue 130 to about amino acid residue 140 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 11 of page 24 as follows:

Human and murine TANGO 273 proteins exhibit considerable sequence similarity, as indicated herein in Figure 1A[[1H]]. Figure 1A[[1H]] depicts an alignment of human and murine TANGO 273 protein amino acid sequences (SEQ ID NOs: 3 and 13, respectively). In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the proteins are 89.5% identical. Alignment of the ORF encoding human TANGO 273 protein and the ORF encoding murine TANGO 273 protein using the same software and parameters indicated that the nucleotide sequences are 84.1% identical.

Please amend the paragraph beginning on line 17 of page 31 as follows:

The full length of the cDNA encoding human TANGO 325 protein (~~Figure 2;~~ SEQ ID NO: 21) is 2169 nucleotide residues. The ORF of this cDNA, nucleotide residues 135 to 2000 of SEQ ID NO: 21

(i.e., SEQ ID NO: 22), encodes a 622-amino acid transmembrane protein (~~Figure 2;~~ SEQ ID NO: 23).

Please amend the paragraph beginning on line 3 of page 36 as follows:

TANGO 325 exhibits amino acid sequence and nucleic acid sequence homology with human Slit-1 protein. An alignment of the amino acid sequences of TANGO 325 and human Slit-1 protein is shown in Figures 2B to 2G~~2G to 2L~~. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4), the proteins are 35.4% identical (i.e., 35.4% of the residues of TANGO 325 correspond to identical residues in Slit-1). An alignment of the nucleotide sequences of the ORFs encoding TANGO 325 and human Slit-1 protein is shown in Figures 2H-1 through 2H-18~~2M-1 through 2M-18~~. The two ORFs are 65.7% identical, as assessed using the same software and parameters.

Please amend the paragraph beginning on line 27 of page 36 as follows:

Figure 2A[[2F]] depicts a hydrophobicity plot of human TANGO 325 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 31 of SEQ ID NO: 23 is the signal sequence of human TANGO 325 (SEQ ID NO: 24). The hydrophobic region which corresponds to amino acid residues 530 to 547 of SEQ ID NO: 23 is the transmembrane domain of human TANGO 325 (SEQ ID NO: 27). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 325 protein from about amino acid residue 550 to about amino acid residue 565 appears to be located at or near the surface of the protein, while the region from about amino acid residue 168 to about amino acid residue 185 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 24 of page 41 as follows:

The full length of the cDNA encoding human TANGO 364 protein (~~Figure 3;~~ SEQ ID NO: 31) is 3510 nucleotide residues. The ORF of this cDNA, nucleotide residues 235 to 1764 of SEQ ID NO: 31

(i.e., SEQ ID NO: 32), encodes a 510-amino acid residue protein (~~Figure 3;~~ SEQ ID NO: 33), corresponding to a 479-residue transmembrane protein. TANGO 364 cDNA can exist in an alternatively-spliced form~~, as listed in Figures 3G through 3I~~. In this alternative form, TANGO 364 cDNA is 2510 nucleotide residues in length (SEQ ID NO: 41). The ORF of this cDNA, nucleotide residues 2 to 898 of SEQ ID NO: 41 (i.e., SEQ ID NO: 42), encodes a 299-amino acid residue protein (~~Figure 3;~~ SEQ ID NO: 43) which has the same sequence as the portions of full length TANGO 364 protein indicated in the alignment (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4) listed in Figures 3B and 3C~~3J and 3K~~. In the discussion which follows, the full length and alternatively-spliced forms of TANGO 364 molecules are referred to individually and collectively as TANGO 364 molecules of the corresponding type (e.g., cDNA and protein).

Please amend the paragraph beginning on line 12 of page 46 as follows:

Figure 3A[[3F]] depicts a hydrophobicity plot of human TANGO 364 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 31 of SEQ ID NO: 33 is the signal sequence of human TANGO 364 (SEQ ID NO: 34), and the hydrophobic region which corresponds to amino acid residues 346 to 370 of SEQ ID NO: 33 is the transmembrane region of TANGO 364 (SEQ ID NO: 37). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 364 protein from about amino acid residue 371 to about amino acid residue 410 appears to be located at or near the surface of the protein, while the region from about amino acid residue 235 to about amino acid residue 245 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 20 of page 49 as follows:

The full length of the cDNA encoding human TANGO 405 protein (~~Figure 4;~~ SEQ ID NO: 51) is 3114 nucleotide residues in length. The open reading frame (ORF) of this cDNA, nucleotide residues 154 to 780 of SEQ ID NO: 51 (i.e., SEQ ID NO: 52), encodes a 209-amino acid residue protein (~~Figure 4;~~ SEQ ID NO: 53), corresponding to a 161-residue secreted protein.

Please amend the paragraphs beginning on line 9 of page 53 as follows:

In PCT Publication No. WO 98/28332, a cDNA encoding murine protein, designated dectin-2, was isolated from dendritic cells and described. Human and murine TANGO 405 proteins exhibit amino acid sequence homology with murine dectin-2. As indicated in the alignment in Figure 4H[[4M]] (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4), human TANGO 405 exhibits about 89.0% sequence identity with murine dectin-2. As indicated in the alignment in Figure 4G[[4L]] (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4), murine TANGO 405 exhibits about 70.3% sequence identity with murine dectin-2.

Another embodiment of a murine TANGO 405 cDNA is shown in ~~Figures 4N to 4P (~~the cDNA having the sequence SEQ ID NO: 71 and the ORF having the nucleotide sequence SEQ ID NO: 72[[)]]. In this embodiment murine TANGO 405 includes a translational frame shift, and the amino acid sequence (SEQ ID NO: 73) of murine TANGO 405 is identical to the amino acid sequence reported for murine dectin-2. These data further confirm that human TANGO 405 is the human ortholog of murine dectin-2.

Please amend the paragraphs beginning on line 5 of page 54 as follows:

Figure 4A[[4D]] depicts a hydrophobicity plot of human TANGO 405 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 48 of SEQ ID NO: 53 is the signal sequence of human TANGO 405 (SEQ ID NO: 54). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 405 protein from about amino acid residue 90 to about amino acid residue 105 appears to be located at or near the surface of the protein, while the region from about amino acid residue 110 to about amino acid residue 120 appears not to be located at or near the surface.

Please amend the paragraphs beginning on line 20 of page 54 as follows:

The full length of the cDNA encoding murine TANGO 405 protein (~~Figure 4;~~ SEQ ID NO: 61) is 821 nucleotide residues, although this cDNA sequence is incomplete. The ORF of this cDNA, nucleotide residues 174 to 707 of SEQ ID NO: 61 (i.e., SEQ ID NO: 62), encodes a protein comprising at least 178 amino acid residues (~~Figure 4;~~ SEQ ID NO: 63).

Please amend the paragraphs beginning on line 3 of page 55 as follows:

Figure 4B[[4G]] depicts a hydrophobicity plot of murine TANGO 405 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 42 of SEQ ID NO: 63 is the signal sequence of murine TANGO 405 (SEQ ID NO: 64). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of murine TANGO 405 protein from about amino acid residue 95 to about amino acid residue 110 appears to be located at or near the surface of the protein, while the region from about amino acid residue 110 to about amino acid residue 120 appears not to be located at or near the surface

Please amend the paragraphs beginning on line 18 of page 55 as follows:

Human and murine TANGO 405 proteins exhibit considerable sequence similarity, as indicated herein in Figure 4C[[4H]]. Figure 4C[[4H]] depicts an alignment of human and murine TANGO 405 amino acid sequences (SEQ ID NOs: 53 and 63, respectively). In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap penalties -12/-4), the proteins are 51.7% identical in the overlapping region (i.e., amino acid residues 1-209 of SEQ ID NO: 53 and amino acid residues 1-178 of SEQ ID NO: 63). The human and murine ORFs encoding TANGO 405 are 74.5% identical in the 541 nucleotide residue overlapping region, as assessed using the same software and parameters and as indicated in Figures 4D[[4I]] through 4F[[4K]]. The nucleotide sequences encoding human and murine TANGO 405 (i.e., SEQ ID NOs: 51 and 61) are about 71.2% identical in the 838 nucleotide residue overlapping region, as assessed using the LALIGN software (Myers and Miller (1989) CABIOS, ver. 2.0; pam120.mat scoring matrix; gap penalties -12/-4).

Please amend the paragraphs beginning on line 26 of page 57 as follows:

The full length of the cDNA encoding human M019 protein (~~Figure 5;~~ SEQ ID NO: 81) is 1202 nucleotide residues. The ORF of this cDNA, nucleotide residues 331 to 585 of SEQ ID NO: 81 (~~Figure 5;~~ SEQ ID NO: 82), encodes a 85-amino acid secreted protein (~~Figure 5;~~ SEQ ID NO: 83).

Please amend the paragraphs beginning on line 18 of page 59 as follows:

Figure 5A[[5C]] depicts a hydrophobicity plot of human M019 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 23 of SEQ ID NO: 83 is the signal sequence of human M019 (SEQ ID NO: 84). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human M019 protein from about amino acid residue 63 to about amino acid residue 80 appears to be located at or near the surface of the protein, while the region from about amino acid residue 55 to about amino acid residue 60 appears not to be located at or near the surface.

Please amend Table A on page 61 as follows:

Table A

Protein Designation	SEQ ID NOs			Depicted in Figure #	ATCC® Accession #
	cDNA	ORF	Protein		
human TANGO 273	1	2	3	1	207185
murine TANGO 273	11	12	13	1	207221
human TANGO 325	21	22	23	2	PTA-147
human TANGO 364	31	32	33	3	PTA-425
human TANGO 364 (alternative form)	41	42	43	3	PTA-425
human TANGO 405	51	52	53	4	PTA-424
murine TANGO 405	61	62	63	4	[[___]]
murine TANGO 405 (alternative form)	71	72	73	4	[[___]]
human M019	81	82	83	5	[[___]]

Please amend the paragraph beginning on line 1 of page 64 as follows:

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having the nucleotide sequence of all or a portion of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, or a complement thereof, or which has a nucleotide sequence comprising one of these sequences, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequences of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~ as a hybridization probe, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook et al., Eds., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring

Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

Please amend the paragraphs beginning on line 23 of page 64 to line 20 of page 65 as follows:

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, or a portion thereof. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize with the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise a portion of a nucleic acid sequence encoding a full length polypeptide of the invention, such as a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of a polypeptide of the invention. The nucleotide sequence determined from cloning one gene allows generation of probes and primers designed for identifying and/or cloning homologs in other cell types, e.g., from other tissues, as well as homologs from other mammals. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions with at least about 15, preferably about 25, more preferably about 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1410, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, or 3500 or more consecutive nucleotides of the sense or anti-sense sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, or of a naturally occurring mutant of any of these sequences.

Please amend the paragraph beginning on line 8 of page 66 as follows:

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, due to degeneracy of the genetic code and thus encode

the same protein as that encoded by the nucleotide sequence of one of SEQ ID NOs: 2, 12, 22, 32, 42, 52, 62, 72, and 82.

Please amend the paragraph beginning on line 27 of page 69 as follows:

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 (25, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, or 3500 or more) nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence, preferably the coding sequence, of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, or a complement thereof. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% (65%, 70%, preferably 75%) identical to each other typically remain hybridized with each other. Such stringent conditions are known to those skilled in the art and can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A example of stringent hybridization conditions are hybridization in 6× sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2× SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, or a complement thereof, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

Please amend the paragraphs beginning on line 10 of page 71 to line 15 of page 72 as follows:

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a polypeptide of the invention that contain changes in amino acid residues that are not essential for activity. Such polypeptides differ in amino acid sequence from any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, yet retain biological activity. In one embodiment, the isolated

nucleic acid molecule includes a nucleotide sequence encoding a protein that includes an amino acid sequence that is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~.

An isolated nucleic acid molecule encoding a variant protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, such that one or more amino acid residue substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

Please amend the paragraphs beginning on line 24 of page 78 to line 22 of page 79 as follows:

Biologically active portions of a polypeptide of the invention include polypeptide regions having an amino acid sequence sufficiently identical to or derived from the amino acid sequence of the protein (e.g., the amino acid sequence shown in any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, or the amino acid sequence encoded by the nucleotide sequence of any of the

clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~), which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding protein. A biologically active portion of a protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of a polypeptide of the invention.

Examples of polypeptides are those which have the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85 or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~. Other useful proteins are substantially identical (e.g., at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85 or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~ and retain the functional activity of the protein of the corresponding naturally-occurring protein. Such proteins can differ in amino acid sequence owing, for example, to natural allelic variation or mutagenesis.

Please amend the paragraph beginning on line 16 of page 84 as follows:

An isolated polypeptide of the invention, or a fragment thereof, can be used as an immunogen to generate antibodies using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polypeptide or protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 10 (preferably 12, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85 or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, and PTA-424~~, ___, and ___~~, and encompasses an epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein.

Please amend the paragraph beginning on line 1 of page 85 as follows:

Examples of epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, e.g., hydrophilic regions. Figures 1B, 1C, 2A, 3A, 4A, 4B and 5A~~1I, 1J, 2F, 3F, 4D, 4G, and 5C~~ are hydrophobicity plots of proteins of the invention. These plots or similar analyses can be used to identify hydrophilic regions.

Please amend the paragraphs beginning on line 26 of page 139 to line 2 of page 140 as follows:

~~A clone encoding murine TANGO 405 was deposited with ATCC® on ___ and was assigned Accession Number ___.~~

~~A clone encoding human M019 was deposited with ATCC® on ___ and was assigned Accession Number ___.~~